

FIGURE 1

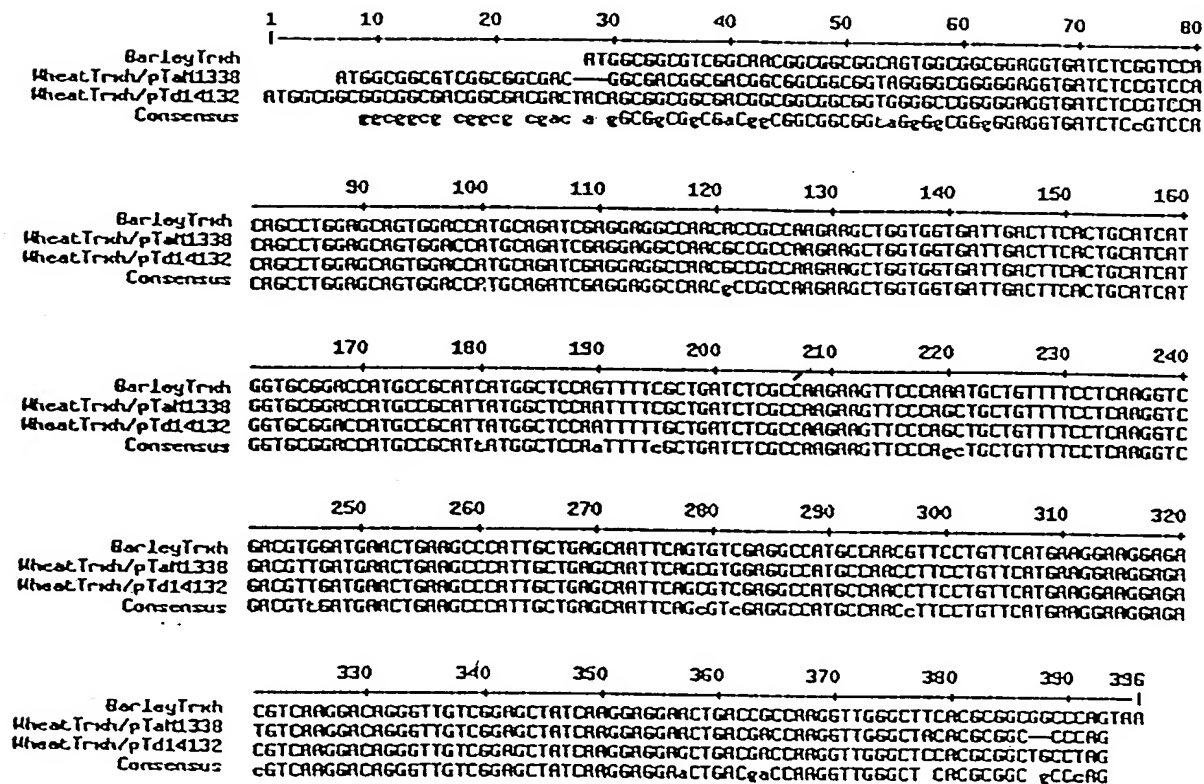
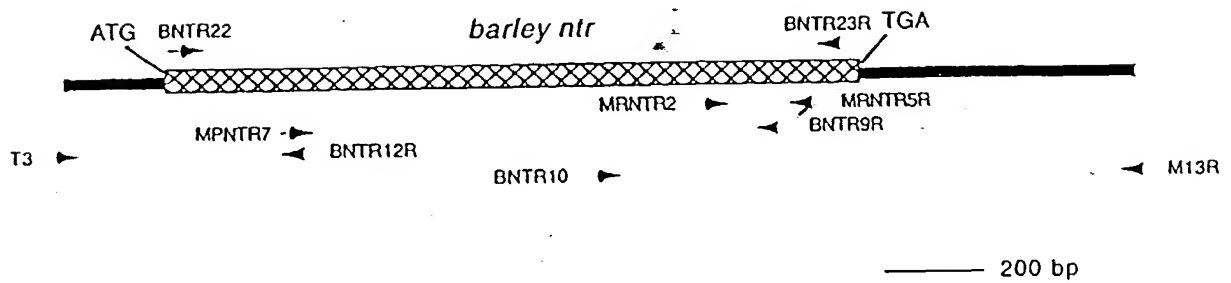


FIGURE 2

### FIGURE 3



## FIGURE 4

A

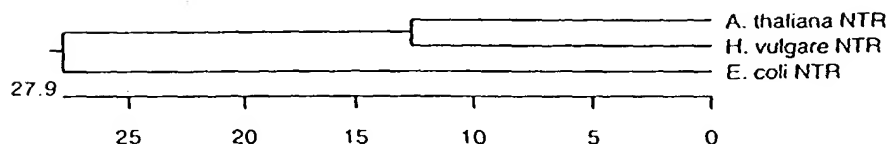
|     |   |                 |
|-----|---|-----------------|
| 1   | MECSAAAPLRTRVCHIGSGPAAHTAATYAARAELKPVLFEGWMANDIAACGQLTVMVE    | H. vulgare NTR  |
| 1   | MNGLETH--NTRICIVGSGPAAHTAATYAARAELKPLIFEGWMANDIAACGQLNOPPR-E  | A. thaliana NTR |
| 1   | MGTTK---HSKILILIGSGPAGYTAAYAAARANIQEVLITC-----MEKCGQLTVMVE    | E. coli NTR     |
| 61  | NFPGFFTGIMCIDLMONCAOSVRECHNLSLSEVTVIEVDFSAEPFVTSDSSTVLACTVW   | H. vulgare NTR  |
| 58  | NFPGFTECHICVELIDKFKOSEREGTTFETETVTKVDFSSKPKIFTDSKAILADAVIL    | A. thaliana NTR |
| 52  | NWPGENDLTCEPLLYERMHEHATKFEFEIFDHINKVQLQNRPPRINGNGEYTDALII     | E. coli NTR     |
| 121 | ATGAVARRIHFSGSDT---YVNRGISACAVCDGAAPIFRNKFLAVICGGDSAMEEGNFI   | H. vulgare NTR  |
| 118 | ATGAVARKWISFVGSSEVLGGLNRRGISACAVCDGAAPIFRNKFLAVICGGDSAMEEGNFI | A. thaliana NTR |
| 112 | ATGASARYILGLPSEEA---FKGRGVSACTGCGF--FYRNQKVAVICGGENTAVEEALYL  | E. coli NTR     |
| 177 | TKYGSQVYLIHRRNTFRASKIMCARALSNPKI-QVVMISEVVEAYCGACGGHLAGVKVN   | H. vulgare NTR  |
| 178 | TKYGSQVYLIHRRNTFRASKIMCARALSNPKI-LVVMNSVVEAYCGACGGHLAGVKVN    | A. thaliana NTR |
| 166 | SNIASQVYLIHRRDCFRASKILIKRLMDKVENGNIILHTNRTLEEVICDQMGVIGVRLRD  | E. coli NTR     |
| 236 | LVTGE-VSDLVVSGLFFAIGHPEATKFLICOLELHAQGVVATKPC-----STHTSVEGVFA | H. vulgare NTR  |
| 237 | VVTGE-VSDLVVSGLFFAIGHPEATKFLICGVELDSQGVVATKPC-----TTOTSVEGVFA | A. thaliana NTR |
| 226 | TQNSNTIESLVVAGLVAIGHSPNTALFEOLELE-NGYIKVQSCIHGNAOTOTSIRGVFA   | E. coli NTR     |
| 291 | AGDVQDKKYROAITAAGSCGMAALDAEHVLOEVGAQVCKSDZ                    | H. vulgare NTR  |
| 292 | AGDVQDKKYROAITAAGTCGMAALDAEHVLOEIGSCQGRSD                     | A. thaliana NTR |
| 285 | AGDVMDHYROAITASATCGMAALDAEFTVDGLADAK                          | E. coli NTR     |

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

B

|                    |      |      |   |                 |  |
|--------------------|------|------|---|-----------------|--|
| Percent Similarity |      |      |   |                 |  |
|                    | 1    | 2    | 3 |                 |  |
| 1                  | 71.4 | 39.3 | 1 | H. vulgare NTR  |  |
| 2                  | 25.4 | 37.4 | 2 | A. thaliana NTR |  |
| 3                  | 55.6 | 56.1 | 3 | E. coli NTR     |  |
|                    | 1    | 2    | 3 |                 |  |

C

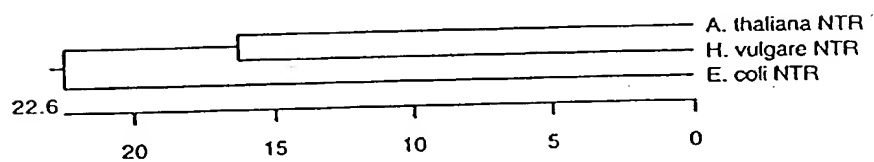


**FIGURE 5**

C

| Percent Divergence | Percent Similarity |      |      |                 |   |
|--------------------|--------------------|------|------|-----------------|---|
|                    |                    | 1    | 2    | 3               |   |
|                    | 1                  |      | 58.2 | 40.5            | 1 |
|                    | 2                  | 32.7 |      | 34.9            | 2 |
|                    | 3                  | 45.3 | 45.0 |                 | 3 |
|                    |                    | 1    | 2    | 3               |   |
|                    |                    |      |      | H. vulgare NTR  |   |
|                    |                    |      |      | A. thaliana NTR |   |
|                    |                    |      |      | E. coli NTR     |   |

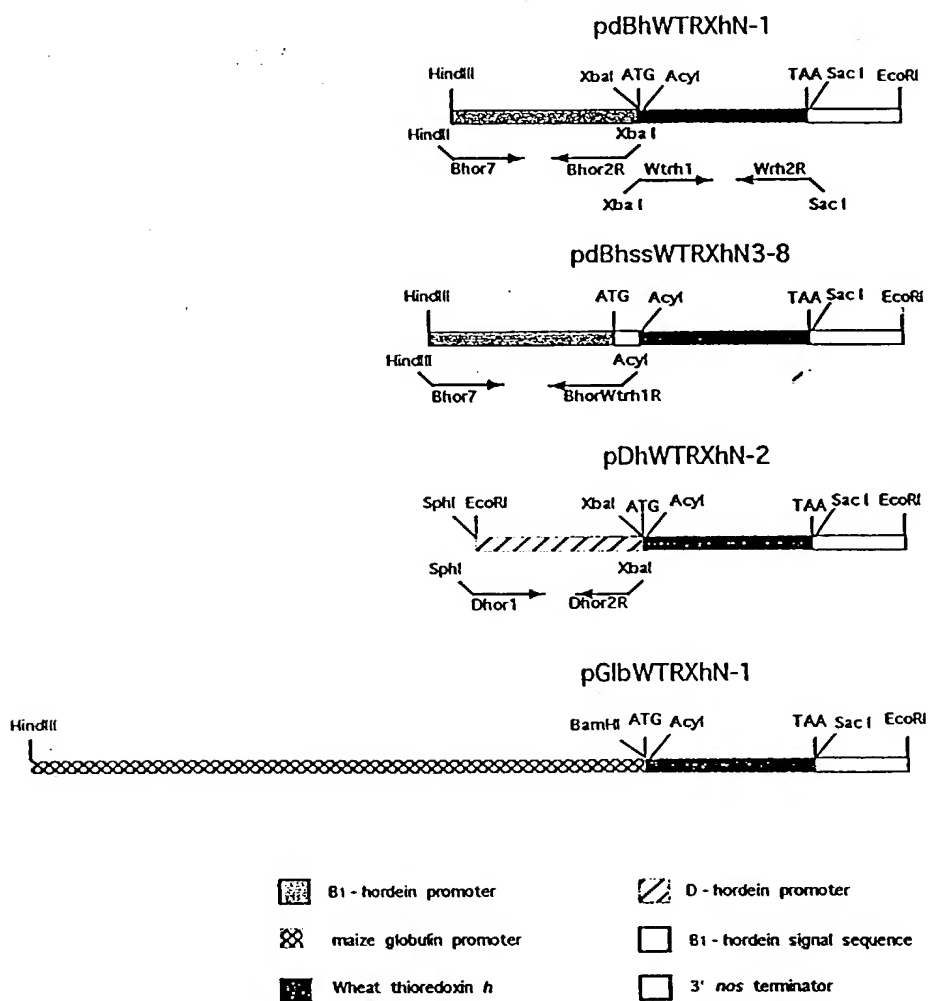
D



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

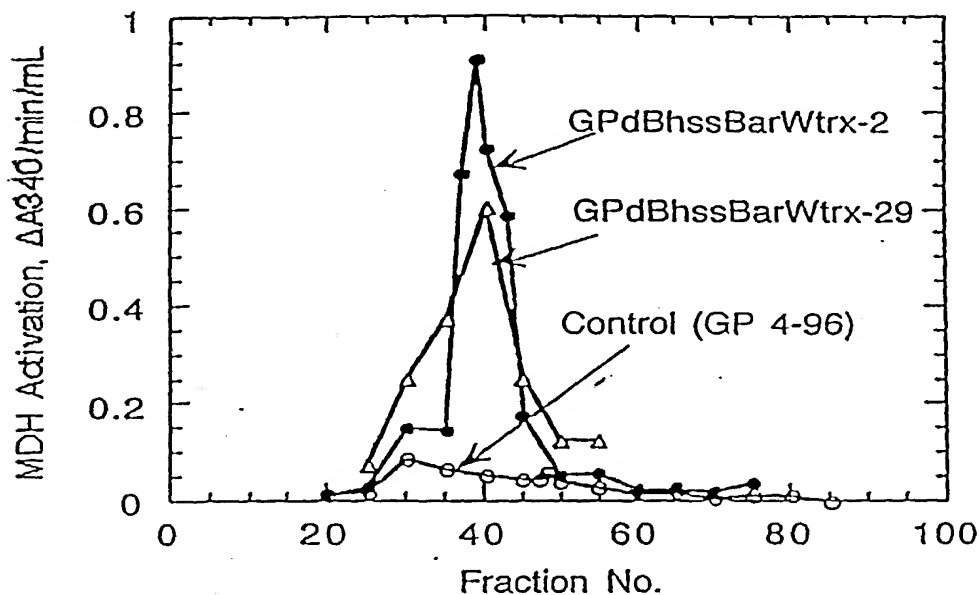
## THIOREDOXIN *h* CONSTRUCTS FOR TRANSFORMATION



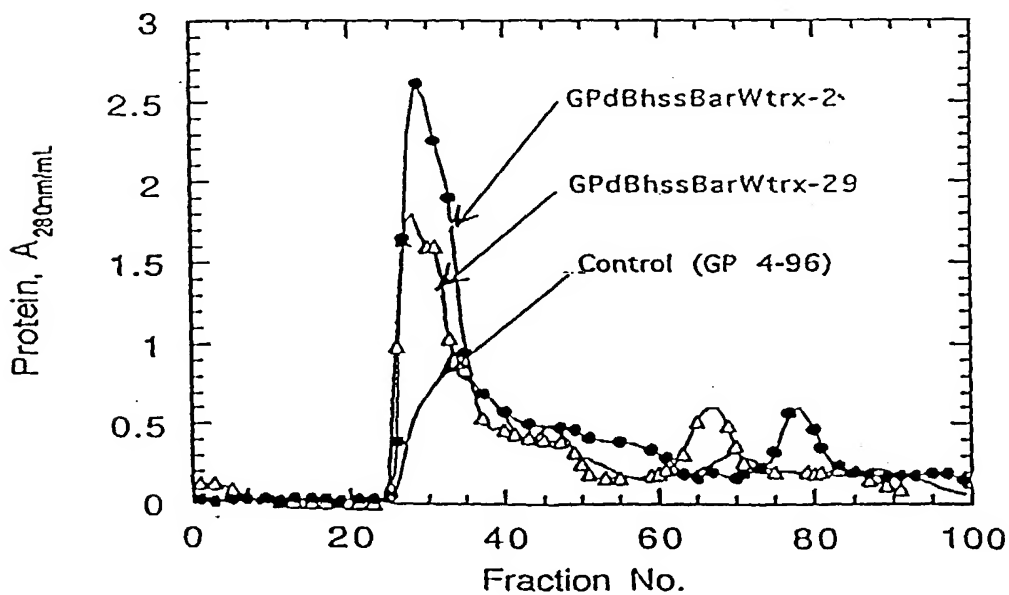
**FIGURE 6**



### Sephadex G-50 Activity Profile of Thioredoxin from Barley Grains (+MDH)



### Sephadex G-50 Elution Profile of Proteins from Three Barley Grains



**FIGURE 7**

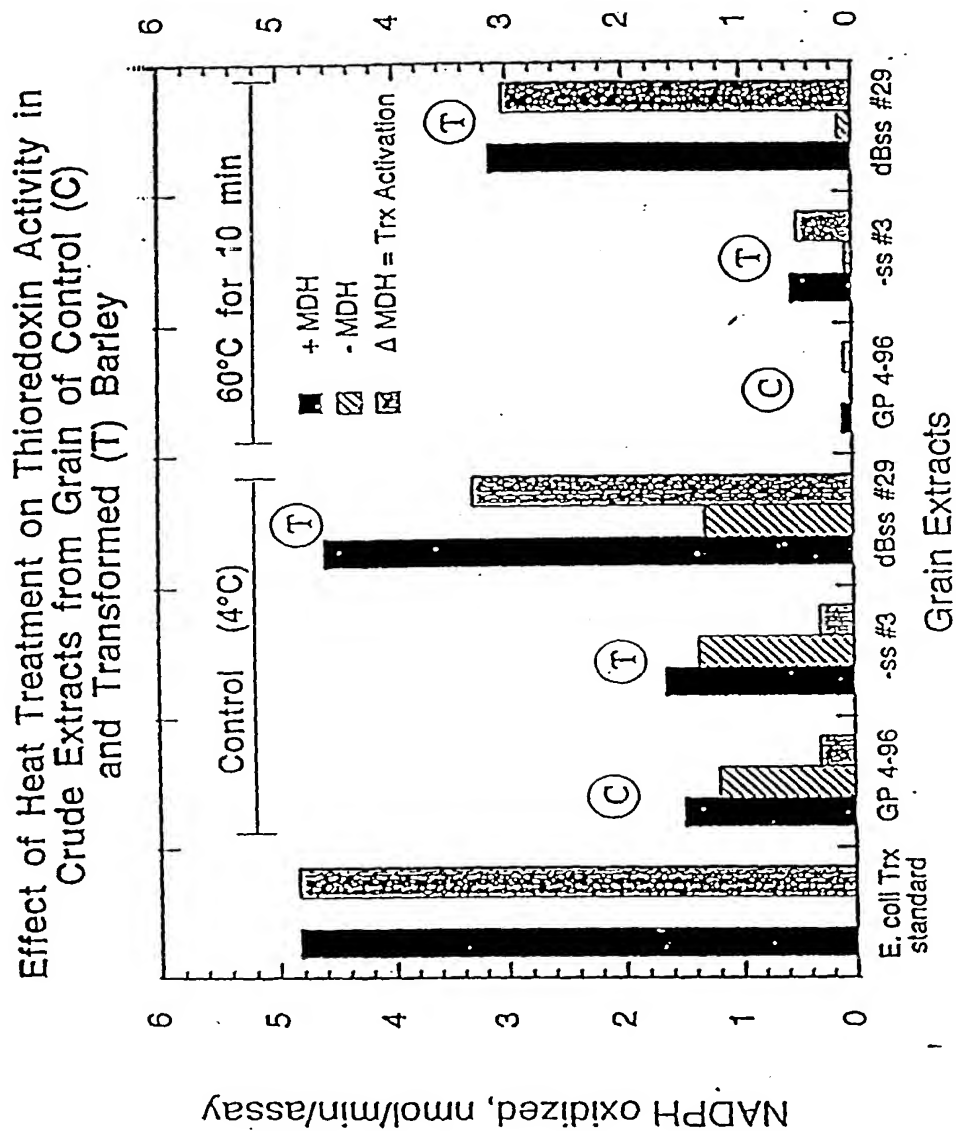
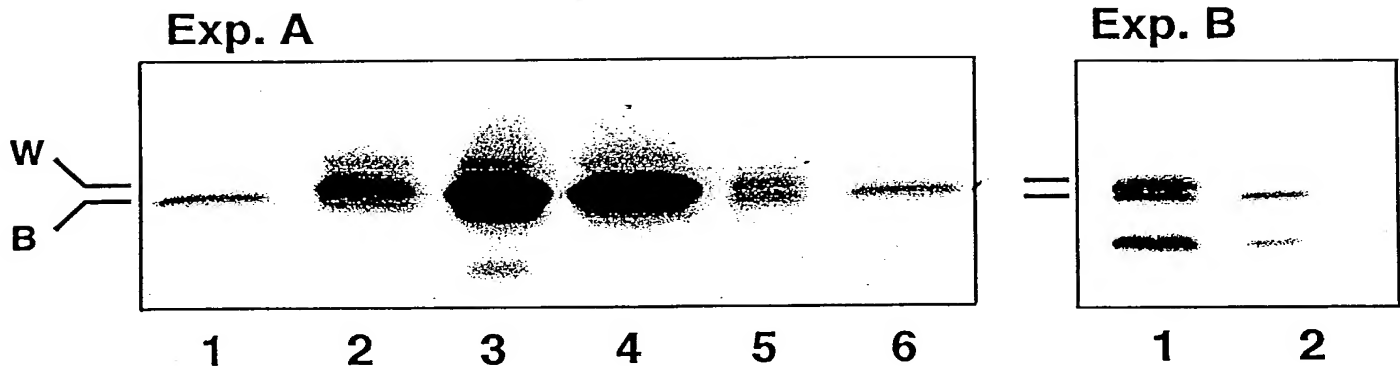


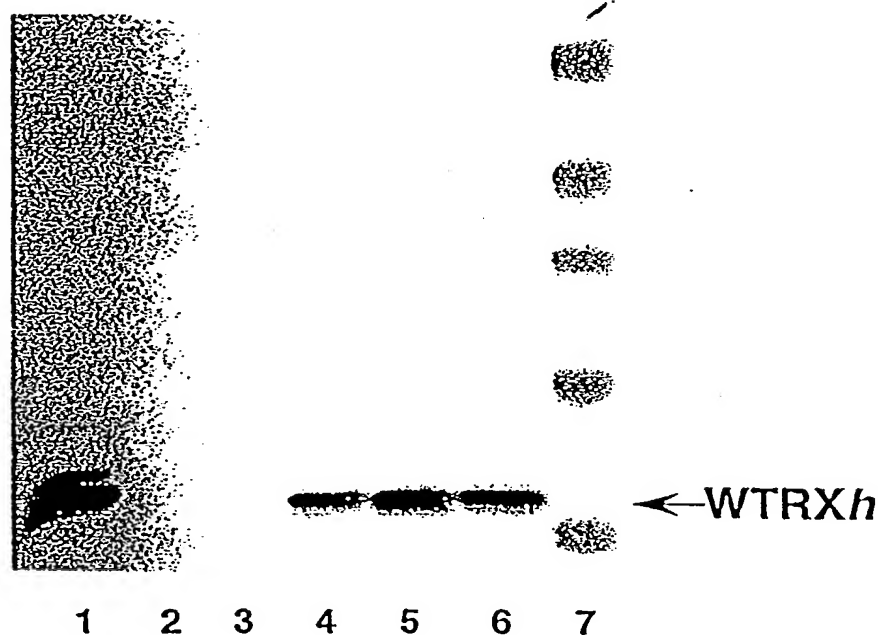
FIGURE 8



**FIGURE 9**

## Western Blot Analysis of Barley Grain Transformed with Wheat Thioredoxin

SDS-PAGE: cv. Golden Promise



1. Wheat germ thioredoxin
2. Control (GP 4-96), nontransformed
3. Control, null segregant (GPdBssBarWtrx-29-11-10)
4. Transformed, heterozygous line (GPdBssBarWtrx-29)
5. Transformed, homozygous line 1 (GPdBssBarWtrx-29-3)
6. Transformed, homozygous line 2 (GPdBssBarWtrx-29-3-2)
7. Prestained standards

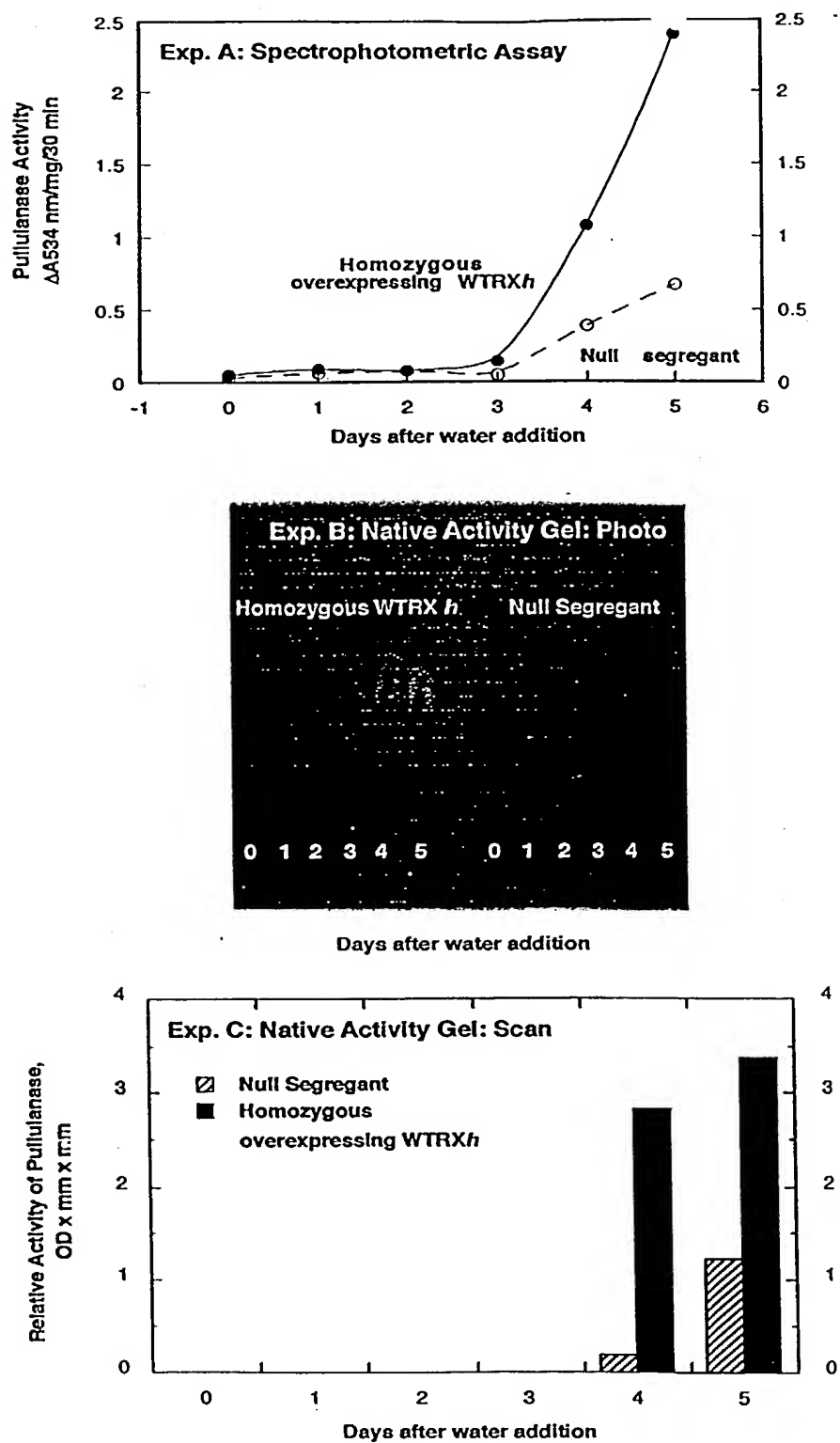
**FIGURE 10**

AAGCTTTAACAACCCACACATTGATTGCAACTTAGTCCTACACAAGTTTTCCATT  
CTTGTTTCAGGCTAACAACCTATACAAGGTTCAAAATCATGCAAAAGTGATGC  
TAGGTTGATAATGTGTGACATGTAAAGTGAATAAGGTGAGTCATGCATACCAAA  
CCTCGGGATTTCTATACTTTGTGTATGATCATATGCACA'ACTAAAGGCAACTTT  
GATTATCAATTGAAAAGTACCGCTTGTAGCTTGTGCAACCTAACACAATGTCCA  
AAAATCCATTTGCAAAAGCATCCAAACACAATTGTTAAAGCTGTTCAAACAAC  
AAAGAAGAGATGAAGCCTGGCTACTATAAATAGGCAGGTAGTATAGAGATCTA  
CACAAGCACAAGCATCAAAACCAAGAAACACTAGTTAACACCAATCCACTATGA  
AGACCTTCCTCATCTTTGCACTCCTCGCCATTGCGGCAACAAGTACGATTGCA

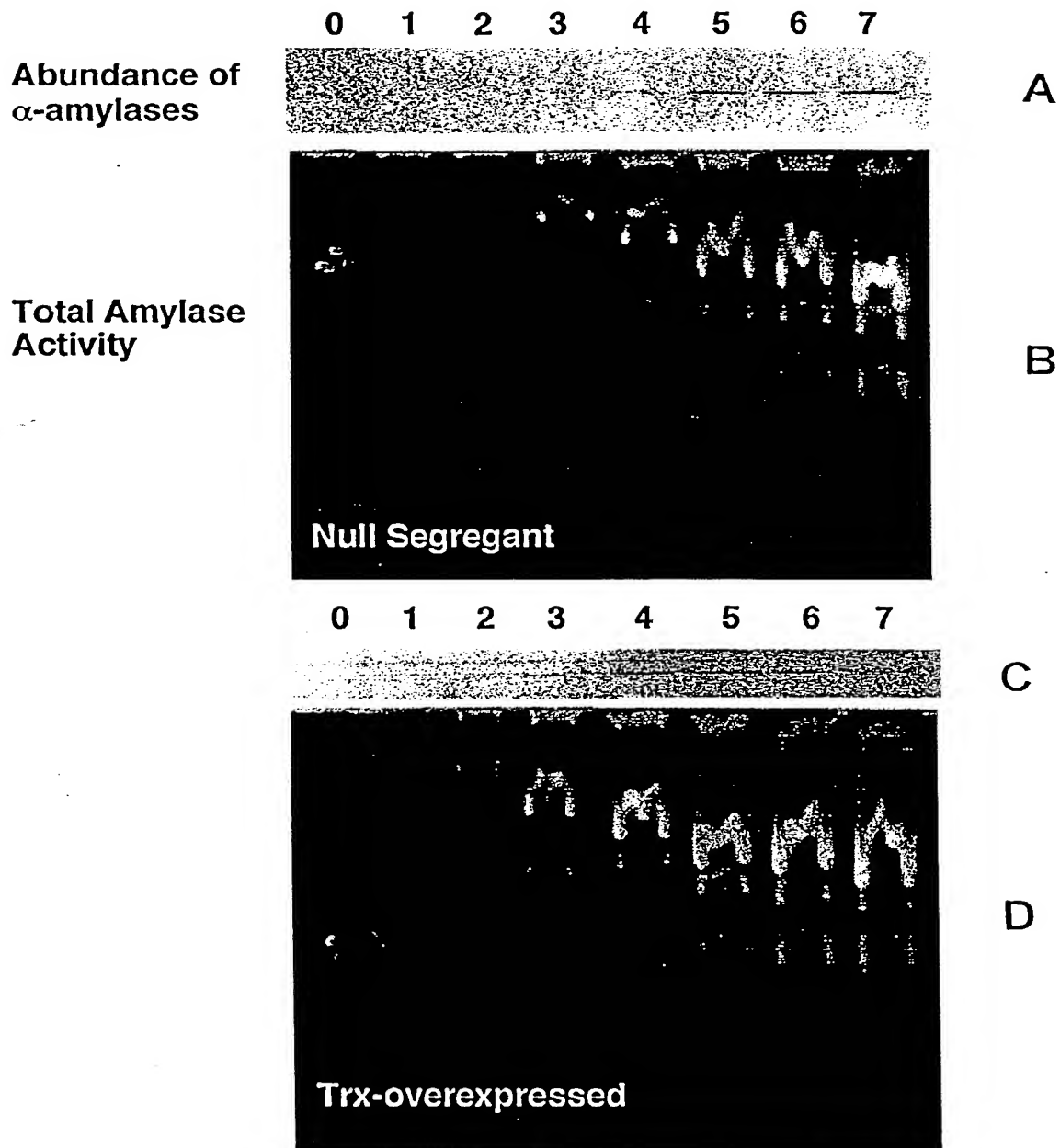
## FIGURE 11

CTTCGAGTGCCCGCCGATTTGCCAGCAATGGCTAACAGACACATATTCTGCC  
AAAACCCCGAACAATAATCACTTCTCGTAGATGAAGAGAACAGACCAAGAT  
ACAAACGTCCACGCTTCAGCAAACAGTACCCCGAAGTATAGGATTAAGCCGAT  
TACGCGGCTTTAGCAGACCGTCCAAAAAAACTGTTTTGCAAAGCTCCAATTCC  
TCCTTGCTTATCCAATTTCTTTTGTGTTGGCAAACCTGCACTTGTCCAACCGATT  
TTGTTCTTCCCGTGTTTCTTCTTAGGCTAACTAACACAGCCGTGCACATAGCC  
ATGGTCCGGAATCTTCACCTCGTCCCTATAAAAGCCCAGCCAATCTCCACAAT  
CTCATCATCACCGAGAACACCGAGAACCAAAAAGTATAGAGATCAATTCATTG  
ACAGTCCACCGAGATGGCTAAGCGGCTGGTCCCTCTTTGTGGCGGTAATCGTC  
GCCCTCGTGGCTCTCACCACCGCT

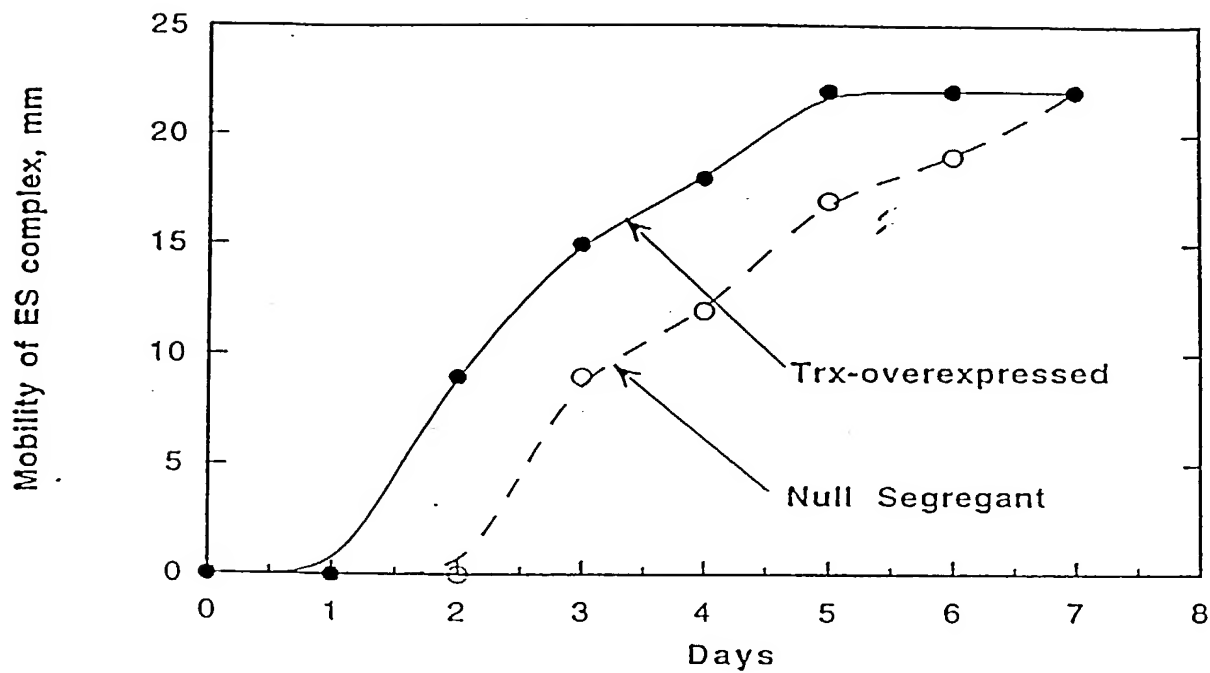
## FIGURE 12

**FIGURE 13**

## FIGURE 14

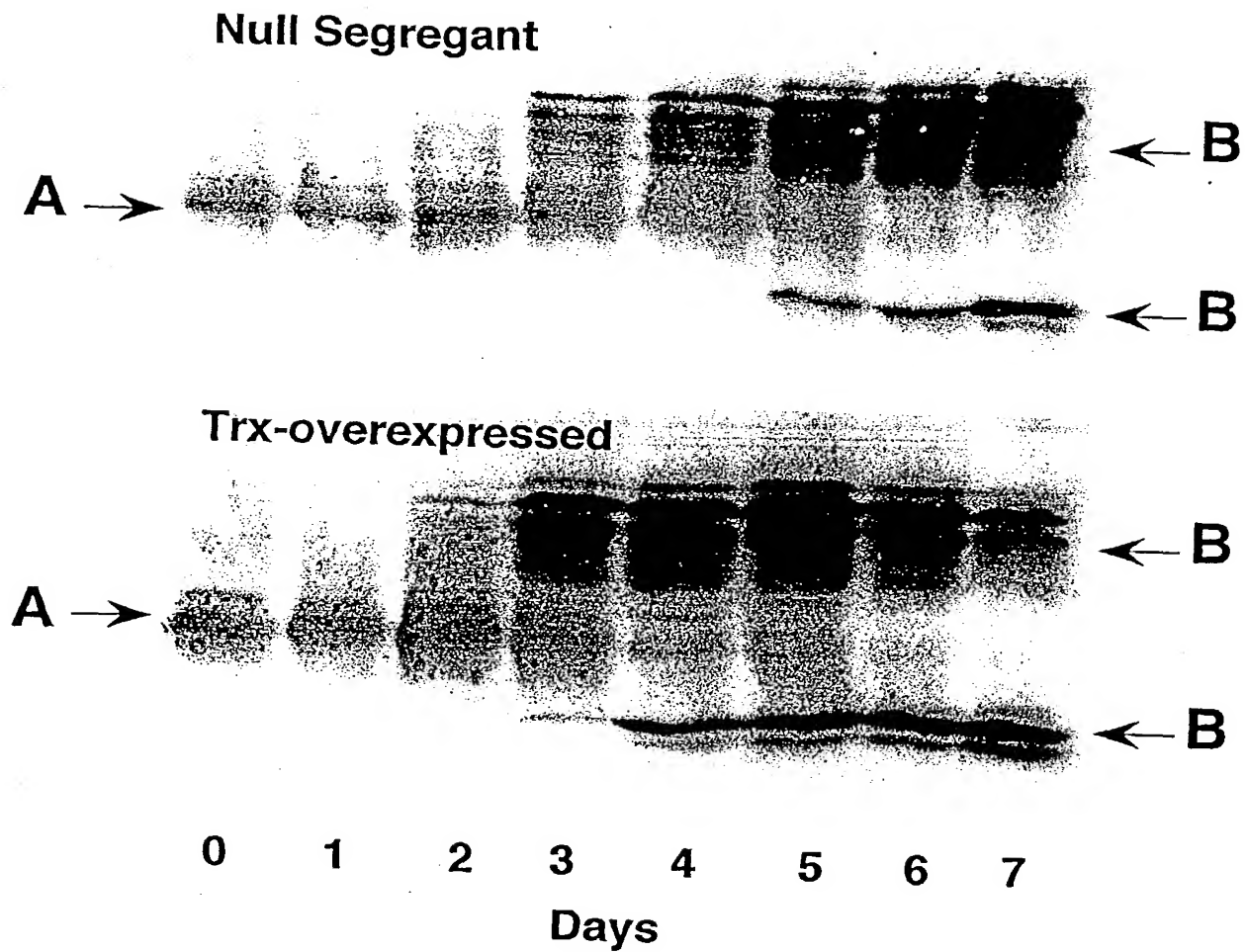


**FIGURE 15**



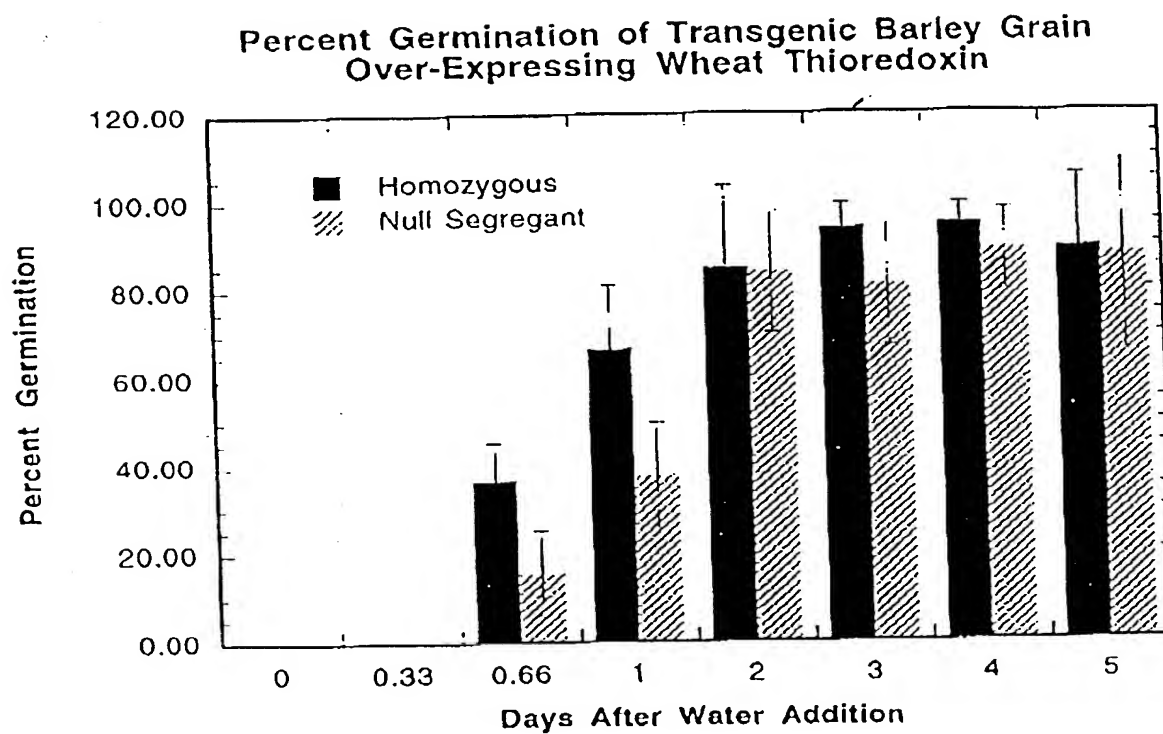


**FIGURE 16A**



**FIGURE 16B**

## FIGURE 17



**FIGURE 18**

**Different Relative Redox Status of Protein Fractions  
in Transgenic Barley Grain Over-Expressing  
Wheat Thioredoxin h vs. the Null Segregant:  
Dry and Germinating Grain**

